TITLE ME Scouching

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	6 466 260.0 mm	&06 280.0 na	707 A	35(.(<u>m</u>	014.5504540	
·:	LVV.V hL	byr.v nt	TCH'A HE	200.4 III.	DNA SEQUENC Microchemistry	
211	0,0068	0.0230 .42	1.8019	0.8541	Requested by Garon South	Data
	0.0471 0.0412	0.0255 1.18	1.84%	0.5429	Notebook Reference requiredy 45 1057	
2/4	0.0531	0.0007 1.03 6.3303 1.30	1.8151 1.7230	0.5569 0.5604	Vector: Please indicate size	For Clones ZO
71 <u>5</u>	(,0078	0.020° .45	1.8048	0.5450	Names of Sample(s): MØ 74- 230	~
216	0.0587	0.0075 L47	1.5785	9.6543	Please provide OD260 and insert size	70 samples) (OD-10 or lute)
217 218	0.0019 0.0002	0.0389 1.30 0.0318 ,96	1.7936 1.7997	0.5577 0.5654		
219	0.0525	0,0299 1.31	1,7548	0.570f		
720	6,0495	0.0288 1-24	1,7194	0.5816		11 Maria - Mar
221	0.0438	0.0292 1.22 0.0349 1.22	1.6709	(१ 985 6. 5 434	a managan and a managan and a same	
2 23	0.0486 0.0271	0.0349 1. 22 0.0187 .6 9	1,8989 1,4499	0.7174 0.8990		DE STATE DES CONTRACTOR DE CON
274	0.0218	0.0158 .55	1,4010	0.7138		
225	0.0380	0.0249 .95	1.528(4.35/5	*****	
22b 2 77	0.0232 0.0357	0.0150 .59 0.0227 .99	1,450T 1,5720	0.8334 0.8381		
228	0.0522	0.0318 1.31	1.8395	0.8998		
554	0.0557	0.0354 L 39	1.5733	0.5550		THE STREET OF THE SECOND SECON
230 X	0.0554	0.0842 1.39	1.8198	0.6174		Anna committee the profession with a financial constitution () and (
MØ ZII MC	i9708	Homo	SAPICAS	c DNA	3' and	94 % (245/260)
MØ 211 MC			sapicos n ABL			94 % (245/760)
212	19709	Huma	n ABL	gene,	intron 16, partial seq.	75% (48/129)
212 213	19709 19710	Huma Lecit	n ABL	gene, desterol	intron 16, partial sequence	75 % (48/129) 100% (283/283)
212 213 214	19709 19210 19211	Huma Lecit Humo	n ABL nin: che in type	gene, plesterol IV co	intron 16, partial sequency layerase mRNA	75 % (48/129) 100% (283/283) 99 % (779/241)
212 213 214 215	19709 !9210 19211 19212	Huma Lecit Huma Huma	n ABL nin: chi in type n nephi	gene, plesterol IV col ropontin	intron 16, partial sequency lagrage mRNA 1 mRNA	75 % (48/129) 100% (283/283) 99 % (779/241) 100% (283/283)
212 213 214 215 216	19709 19210 19211 19212 19213	Huma Lecit Huma Huma Gangi	n ABL nin: cho nin type n nepho side G	gene, plesterol IV col ropontion Mz act	intron 16, partial sequency lagrage mRNA 1 mRNA Valor precursor (human)	75 % (48/129) 100% (283/283) 94 % (774/281) 100% (283/283) 96% (236/244)
212 213 214 215	19709 !9210 19211 19212	Huma Lecit Huma Huma Gangi	n ABL nin: chi in type n nephi	gene, plesterol IV col ropontion Mz act	intron 16, partial sequency lagrage mRNA 1 mRNA Valor precursor (human)	75 % (48/129) 100% (283/283) 99 % (779/241) 100% (283/283) 96% (236/244)
212 213 214 215 216	19709 19210 19211 19212 19213	Huma Lecit Huma Huma Gangii Human	n ABL nin: chi nin type n nephi side G nephi	gene, plesterol IV col ropontin MZ act	intron 16, partial sequescy hours ferase lagenase mRNA n mRNA ivator precursor (human) mRNA	75 % (48/129) 100% (283/283) 94 % (774/281) 100% (283/283) 96% (236/284) 99% (281/283)
212 213 214 215 216 217	19709 19210 19211 19212 19213 19214	Huma Lecit Huma Huma Gangii Human	n ABL nin: cho nin type n nepho side G	gene, plesterol IV col ropontin MZ act	intron 16, partial sequescy hours ferase lagenase mRNA n mRNA ivator precursor (human) mRNA	75 % (48/129) 100% (283/283) 94 % (774/281) 100% (283/283) 96% (283/283) 96% (281/283)
212 213 214 215 216 217 216	19709 19210 19211 19212 19213 19214	Huma Lecit Huma Huma Gangi Human	n ABL nin: chi nin type n nephi side G nephi nglyco	gene, plesterol TV col ropontin Mz ach ropontin protein	intron 16, partial sequescy hours ferase lagenase mRNA n mRNA water precursor (human) mRNA mRNA mRNA	75 % (48/129) 100% (283/283) 94 % (779/241) 100% (283/283) 96% (283/283) 96% (236/244) 99% (281/283) 68% (178/258)
212 213 214 215 216 217 216 219 220	19709 19210 19211 19212 19213 19214 19215	Huma Lecit Huma Huma Gangi Human	n ABL nin: chi nin type n nephi side G nephi nglyco	gene, plesterol TV col ropontin Mz ach ropontin protein	intron 16, partial sequescy hours ferase lagenase mRNA n mRNA ivator precursor (human) mRNA	75 % (48/129) 100 % (283/283) 94 % (779/281) 100% (283/283) 96 % (283/283) 96 % (281/283) 68 % (178/258)
212 213 214 215 216 217 216 219 220 221	19709 19210 19211 19212 19213 19214 19215	Huma Lecit Huma Huma Human Human	n ABL nin: chi nin type n nephi nide G nophi n glyco n nephi	gene, plesterol TV col ropontin protein roponti	intron 16, partial sequescy human sequences mRNA mRNA mRNA mRNA mRNA mRNA mRNA mRNA	75 % (48/129) 100 % (283/283) 94 % (774/281) 100 % (283/283) 96 % (283/283) 96 % (286/284) 99 % (286/283) 68 % (178/258)
212 213 214 215 216 217 216 219 220 221	19709 19210 19211 19212 19213 19214 19215	Huma Lecit Huma Huma Gangi Human Huma Human	n ABL nin: chi nin: chi	gene, plesterol IV col repontin protein repontin	intron 1b, partial sequency lagrage mRNA mRNA mRNA mRNA mRNA mRNA mRNA mRNA mRNA	75 % (48/129) 100 % (283/283) 94 % (774/281) 100 % (283/283) 96 % (283/283) 96 % (281/283) 68 % (281/283) 68 % (178/258) 99 % (275/280)
212 213 214 215 216 217 216 219 220 221 222 223	19709 19710 19211 19213 19214 19215 19217	Huma Lecit Huma Huma Gangii Human Huma Huma Huma	n ABL nin: chi nin type n nephi side G nophi n glyco n nephi sapici	gene, plesterol IV col ropontin Mz acl ropontin protein roponti	intron 1b, partial sequency lagrage mRNA A clone 53126 3'	75 % (48/129) 100% (283/283) 94 % (779/241) 100% (283/283) 96 % (284/283) 96 % (281/283) 68 % (281/283) 68 % (178/258) 98 % (275/280) 99 % (98/109) 97 % (98/109)
212 213 214 215 216 217 216 219 220 221	19709 19210 19211 19212 19213 19214 19215	Huma Lecit Huma Huma Gangii Human Huma Huma Huma	n ABL nin: chi nin: chi	gene, plesterol IV col ropontin Mz acl ropontin protein roponti	intron 1b, partial sequency lagrage mRNA A clone 53126 3'	75 % (48/129) 100 % (283/283) 94 % (774/281) 100 % (283/283) 96 % (283/283) 96 % (281/283) 68 % (281/283) 68 % (178/258) 99 % (275/280) 99 % (98/109) 97 % (88/90)
212 213 214 215 216 217 216 219 220 221 222 223 224	19709 19710 19211 19213 19214 19215 19217 19217 19219 19220 19221	Huma Lecit Huma Huma Gangii Huma Huma Huma Huma Huma	n ABL nin: chi nin type n nephi side G nophi n glyco n nephi sapici	gene, plesterol IV col ropontin Mz acl ropontin protein roponti	intron 1b, partial sequency lagrage mRNA A clone 53126 3'	75 % (48/129) 100% (283/283) 94 % (779/241) 100% (283/283) 96 % (284/283) 96 % (281/283) 68 % (281/283) 68 % (178/258) 98 % (275/280) 99 % (98/109) 97 % (98/109)
212 213 214 215 216 217 216 219 220 221 272 223	19709 19710 19211 19213 19214 19215 19217 19217 19219 19220 19221	Huma Lecit Huma Huma Gangii Huma Huma Huma Huma Huma	n ABL nin: chi nin type n nephi side G nophi n glyco n nephi sapici	gene, plesterol IV col ropontin mz ach ropontin protein ropontin ropontin ropontin	intron 1b, partial sequency lagrage mRNA A clone 53126 3'	75 % (48/129) 100% (283/283) 99 % (779/281) 100% (283/283) 96 % (281/283) 98 % (281/283) 68 % (178/258) 99 % (275/280) 99 % (48/109) 99 % (279/281)

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cc:Mail for: heather pearson

Subject: No subject given P Forwarded: JEFF GARDIN

To: Heather Pearson

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To: Aaron_Smith_at_ICOS-Science@icos.com
 Subject: Re: 19215
 gb | M80927 | HUMHA3G
                   Human glycoprotein mRNA, complete cds.
                                                             4.8e-40
                                                        572
 gb|U19900|SSU19900
                   Sus scrofa 38kDa heparin-binding gly...
                                                        546
                                                             7.1e-38
 gb R55530 R55530
                   yj79c12.rl Homo sapiens cDNA clone 1...
                                                        368
                                                             2.3e-21
 dbj | D32218 | HAMOSG
                   Hamster mRNA for oviduct-specific gl...
                                                        271
                                                             8.1e-13
 gb|U09550|HSU09550
                   Human oviductal glycoprotein mRNA, c...
                                                             1.8e-12
                                                        267
 gb|U17988|QAU17988
                   Ovis aries 92kD oestrus-associated o...
                                                        235
                                                            9.0e-10
 dbj|D16639|BOV95BOGP Bovine mRNA for 95 kDa oviduct-speci...
                                                        217
                                                             3.1e-08
 gb U15048 MAU15048
                   Mesocricetus auratus oviductin mRNA,...
                                                        211 1.0e-07
 gb R03212 R03212
                   pk05a03.s1 Caenorhabditis briggsae c...
                                                        201
                                                            4.5e-07
 gb U13646 CELZK783
                   Caenorhabditis elegans cosmid ZK783.
                                                        129
                                                            0.58
 gb|T92100|T92100
                   ye01h11.rl Homo sapiens cDNA clone 1...
                                                        123 0.91
 >gb|M80927|HUMHA3G Human glycoprotein mRNA, complete cds.
           Length = 1741
  Plus Strand HSPs:
 Score = 572 (158.1 bits), Expect = 4.8e-40, P = 4.8e-40
 Identities = 178/258 (68%), Positives = 178/258 (68%), Strand = Plus / Plus
         24 CAGGTTTCATGGTCCTGCTGATGATCCCATGGGGCTCTGCTGCTACAAAACTGGTCTGCTACT 83
                   1111111111111
Sbjct:
         94 CAGGCTTTGTGGTCCTGGTGCTCCAGTGCTGCTCTGCATACAAACTGGTCTGCTACT 153
         84 TCACCAACTGGGCCCAGTACAGACAGGGGGGGGGGGGTCGCTTCCTGCCCAAGGACTTGGACC 143
Query:
             Sbjct:
        154 ACACCAGCTGGTCCCAGTACCGGGAAGGCGATGGGAGCTGCTTCCCAGATGCCCTTGACC 213
Query:
        214 GCTTCCTCTGTACCCACATCATCTACAGCTTTGCCAATATAAGCAACGATCACATCGACA 273
Sbjct:
Query:
        204 CCACTGAGTGGAATGACGAGACTCTCTACCAGGAGTTCAATGGCCTGAAGAAGATGAATC 263
                Sbjct:
        274 CCTGGGAGTGGAATGATGTGACGCTCTACGGCATGCTCAACACACTCAAGAACAGGAACC 333
Query:
        264 CCAAGCTGAAGACCCTGT 281
            111 11111111 11 1
Sbict:
        334 CCAACCTGAAGACTCTCT 351
>gb|U19900|SSU19900 Sus scrofa 38kDa heparin-binding glycoprotein mRNA,
           complete cds. >emb|Z47803|SSGP38KD S.scrofa 38kDa heparin-binding
          glycoprotein.
          Length = 1733
  Plus Strand HSPs:
 Score = 546 (150.9 bits), Expect = 7.1e-38, P = 7.1e-38
 Identities = 184/278 (66%), Positives = 184/278 (66%), Strand = Plus / Plus
Query:
         2 ATGGTGCGGTCTGTGGCCTGGGCAGGTTTCATGGTCCTGATGATCCCATGGGGCTCT 61
                             1 1111111
            1111
                      1111
                                       111 111 11 11 11 11
Sbjct:
         67 ATGGGTCTGAGGGTGGCTCAGACAGGTTTTGTGGCCCTGGTGCTGCTCCAGAGCTGTGCT 126
Query:
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